AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph on page 13, line 22 with the following amended paragraph:

Peptides of the invention were confirmed to be epitope peptides recognized by cytotoxic T lymphocytes (hereinafter referred to as "CTL") as a result of screening potential peptides to be epitope peptides with reference to the HLA Peptide Binding Predictions, BioInformatics & Molecular Analysis Section (BIMAS), (~~http://~~bimas.dcrt.nih.gov/molbio/hla_bind/index.html), which is a reference site for searching epitope peptides consisting of 9 to 10 amino acids having an HLA-A2402-binding motif in amino acid sequences derived from the Ep-CAM protein widely expressed on cancer cells originating from epithelial cells.

Please replace the paragraph on page 34, line 18 with the following amended paragraph:

A large cell carcinoma cell line LU 99 (JCRB0080) as a human lung cancer cell line; a human epidermoid carcinoma cell line HSC-2 (JCRB0622); epidermoid carcinoma cell lines MKN28 (JCRB0253) and MKN45 (JCRB0254) as a human gastric cancer cell line; and an epidermoid carcinoma cell line COLO320DM (JCRB0225 or ATCC:CCL -220) as a human colorectal cancer cell line were purchased from the JCRB Cell bank (Ministry of Health, Labour and Welfare: ~~http//~~Cellbank.nihs.go.jp). An epidermoid carcinoma cell line LC-1/sq (RCB0455) as a human lung cancer cell line was purchased from the Riken cell bank.

Please replace the paragraph on page 35, line 26 with the following amended paragraph:

Potential HLA-A2402-binding peptides within Ep-CAM (accession number: M33011) were identified by computer-based prediction according to the HLA Peptide Binding Prediction Program based on the estimated half-time dissociation of HLA peptide complexes available at the World Wide Website Bioinformatics & Molecule Analysis Section (BIMAS:BioInfomatics and molecular analysis section) (~~http://~~bimas.dcrt.gov/molbio/hla_bind).

Please replace Table 1 at page 36, with the following amended Table 1:

Table 1

Peptide name	Amino acid sequence	Amino acid positions	Amino acid length	Score[a]	%MFI increase[b]
Ep_{31}	NYKLAVNCF (SEQ ID NO:3)	31-39	9	120	85
Ep_{173}	RYQLDPKFI (SEQ ID NO:1)	173-181	9	150	102
Ep_{185}	LYENNVITI (SEQ ID NO:4)	185-193	9	75	79
Ep_{225}	LFHSKKMDL (SEQ ID NO:5)	225-233	9	20	29
Ep_{250}	YYVDEKAPEF (SEQ ID NO:2)	250-259	10	198	57
Ep_{296}	KYEKAEIKEM (SEQ ID NO:6)	296-305	10	83	24
Ep_{304}	EMGEMHREL (SEQ ID NO:7)	304-312	9	5	16

Please replace the paragraph on page 36, lines 13-18 with the following amended paragraph:

Separately, human immunodeficiency virus-1 (HIV-1) envelope peptide RYLRDQQLL (SEQ ID NO:13) (designated ENV584, J. Immunol, 159:6242-6252, 1997: residues 584-592) and EBV latent membrane protein 2 peptide (EBV latent membrane) (designated EBV-LMP419, J. Immnol, 158:3325-3334, 1997: residues 419-427) were synthesized as controls (Toray Industries research center company).